

D1
CONT

and/or chromosome 17 in humans, said method comprising [contacting] employing said chromosomal material [with] and a unique sequence high complexity nucleic acid probe of greater than about 50,000 bases in in situ hybridization, wherein the chromosomal material is present in a morphologically identifiable chromosome or cell nucleus; allowing said probe to bind to said targeted chromosomal material; and detecting said bound probe, wherein bound probe is indicative of the presence of target chromosomal material.

D2
SUB
E3

48. (Amended) A method of staining targeted interphase chromosomal material based upon a nucleic acid segment employing a unique sequence high complexity nucleic acid probe of greater than about 40 kb, wherein said targeted chromosomal material is a genetic rearrangement associated with chromosome 3 and/or chromosome 17 in humans, said method comprising contacting said chromosomal material with a unique sequence high complexity nucleic acid probe of greater than about 40 kb, wherein the chromosomal material is present in a morphologically identifiable chromosome or cell nucleus; allowing said probe to bind to said targeted chromosomal material; and detecting said bound probe, wherein bound probe is indicative of the presence of target chromosomal material.

D3
SUB
E3

50. (Amended) A method of staining targeted interphase chromosomal material based upon a nucleic acid segment employing a unique sequence high complexity nucleic acid probe of greater than about 50,000 bases, wherein said targeted interphase chromosomal material is a genetic rearrangement associated with chromosome 3 and/or chromosome 17 in humans, said method comprising contacting said interphase

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chromosomal material with a unique sequence high complexity nucleic acid probe of greater than about 50,000 bases, wherein the chromosomal material is present in a morphologically identifiable chromosome or cell nucleus; allowing said probe to bind to said targeted interphase chromosomal material; and detecting said bound probe, wherein bound probe is indicative of the presence of target interphase chromosomal material.

L Please add new claims as follows:

4 --~~51~~². The method of claim ~~48~~², wherein the genetic rearrangement is a translocation or an inversion.

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5 ~~52~~². The method of claim ~~48~~², wherein the unique sequence high complexity nucleic acid probe is labeled.

6 ~~53~~⁵. The method of claim ~~52~~⁵, wherein said labeled unique sequence high complexity nucleic acid probe comprises fragments complementary to a single chromosome, fragments complementary to a subregion of a single chromosome, fragments complementary to a genome or fragments complementary to a subregion of a genome.

7 ~~54~~². The method of claim ~~48~~², wherein the interphase chromosomal material is interphase chromosomal DNA.

8 ~~55~~³. The method of claim ~~50~~³, wherein the genetic rearrangement is a translocation or an inversion.

9 ~~56~~³. The method of claim ~~50~~³, wherein the unique sequence high complexity nucleic acid probe is labeled.